CLAIMS

1. A method for obtaining signature probes comprising the steps of:

A. Compiling a database of nucleic acid sequences from a substantially homologous region of an RNA or DNA comprising sequences from all organisms or viruses that will be incorporated into the analysis;

B. Compiling a bifurcating tree that shows the genetic relationships between the organisms whose nucleic acid sequences will be included in the analysis;

C. Calculating the occurrence frequency and distribution of every oligoribonucleotide or oligodeoxyribonucleotide sequence of length N in the sequence database;

D. Calculating a signature quality function which measures the extent to which each particular oligoribonucleotide or oligodeoxyribonucleotide sequence of length N is characteristic of each node in a substantially bifurcating substantially phylogenetic tree of genetic relationships;

E. Selecting a oligoribonucleotide or oligodeoxyribonucleotide sequenceas a signature for a particular node if the quality index for said sequence has its greatest value for that node and the quality index exceeds a preset value;

F. Synthesizing signature probes appropriate for use in a hybridization experiment that incorporate the node-specific information of the signature sequences.

2. A method of claim 1 in which the signature quality index varies from 0.0 to 1.0 and the preset value is chosen to be greater than 5..

3. A method of claim 1 in which the signature quality index Qs is calculated by substantially the equation:

$$Q_s = (N_{GM} / N_{GT}) \times (1 - (N_M - N_{GM}) / N_M)$$
$$= (N_{GM}^2) / (N_{GT} \times N_M)$$

in which where N_M is the number of probe-matched organisms in the entire tree, N_{GM} is the number of probe-matched organisms in the group of interest, and N_{GT} is the number of organisms in the group under consideration.

4. A method of determining the genetic affinity of organisms or viruses in a test sample comprising the steps of:

A. Deriving a plurality of nucleic acid signature probes from a database of signature sequences that are able to hybridize to only a portion of the nucleic acid sequence of the organism or virus.

B. Hybridizing the signature probes to the nucleic acid obtained from the test sample under hybridization conditions to cause those signature probes that are complementary to hybridize to the nucleic acid of the organism or virus and produce a detectable signal.

C. Tabulating which signature probes produce a detectable hybridization signal.

D. Identifying the closest known genetic relatives of the organism or virus in the test sample by determining which nodes in the bifurcating tree of genetic relationship that was used to design the signature probes that produced the hybridization signal.

E. Identifying the organism or virus in the test sample as being contained within the most terminal node that is supported by one or more positive signature probes.

5. A method of claim 4 wherein the signature probes are comprised of a moiety selected from the group consisting of: RNA, DNA, an analog of RNA or DNA including peptide nucleic acids, 2-O-methyl DNA or any other molecule that can interact with the test sample nucleic in a sequence- specific way..

6. A method of claim 4 wherein the hybridization step utilizes a feature selected from the group consisting of:an immobilized array of signature probes, molecular beacons, hybridization step done in solution.

7. A method of claim 4 wherein the detection step utilizes radioactive labels, chemiluminescence and/or fluorescence.

8. A method of claim 4 wherein a tree of relationships signifying genetic relationship is generated by a standard method selected from the group consisting of parsimony methods, distance methods, and maximum likelihood.

9. A method of claim 4 wherein the most narrowly defined groupings on the tree of relationship comprises a moiety selected from the group consisting of: a specific genera, a specific species, a race, serotype, type or other grouping below the species level.

10. A method of claim 4 in which the signature probes are constructed by the method of claim 1.

11.. A method of devising oligonucleotide probes for use in hybridization comprising using the sequence information provided in a signature sequence to construct the probe

12. An isolated nucleic acid molecule comprising the sequence shown in Table B.

13. The RNA sequence CUGCAGAGAUGA or the corresponding DNA sequence, and probes complementary to any of the foregoing or to sequences containing any of the foregoing, which are valuable for identification of samples containing organisms with strong genetic affinity to Legionella nautarum.

14. The RNA sequence AAAAUCAUUCUC or the corresponding DNA sequence, and probes complementary to any of the foregoing or to sequences containing any of the foregoing, which are valuable for identification of samples containing organisms with strong genetic affinity to specific for organisms with strong genetic affinity to Listeria gray.

15. The RNA sequence CGGGAGGCAGCAGCU or the corresponding DNA sequence, and probes complementary to any of the foregoing or to sequences containing any of the foregoing, which are valuable for identification of samples containing organisms selected from the group of genera consisting of Borrelia, Brachyspira, Spirochaeta and Treponema.

16. The RNA sequence AUUACAAACUGU or the corresponding DNA sequence, and probes complementary to any of the foregoing or to sequences containing any of the foregoing, which are valuable for identification of samples containing organisms with strong genetic affinity to Ureaplasma canigenitalium.

17. The RNA sequence GGAGGAUGAAGGUUU and GGCGACCUGCUGGAA which are substantially perfect signatures for node 4254 which contains various members of the genus Helicobacter and GGCGUGCGAGCGUGG which is a substantially perfect signature for node 3634 which contains species of Isosphaera

18. An assay or test kit comprising an RNA sequence selected from the group consisting of AAAAUCAUUCUC, CGGGAGGCAGCAGCU, AUUACAAACUGU, GGAGGAUGAAGGUUU and GGCGACCUGCUGGAA or the corresponding DNA sequence, and probes complementary to any of the foregoing or to sequences containing any of the foregoing

19. A method of claim 4 in which the signature probes are of length 6 or larger and where the nucleic acid is DNA isolated from the spacer region between ribosomal RNA genes or a fragment of the foregoing;

20. All inventions contained herein.